



IFWO

RAW SEQUENCE LISTING

DATE: 02/20/2004

PATENT APPLICATION: US/10/645,012

TIME: 14:42:41

Input Set : N:\Crf3\RULE60\10645012.RAW.txt

Output Set: N:\CRF4\02202004\J645012.raw

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1 <110> APPLICANT: Tsuchiya, Masayuki
2      Saito, Mikiyoshi
3      Ohtomo, Toshihiko
4 <120> TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
5 <130> FILE REFERENCE: 06501-070001
6 <140> CURRENT APPLICATION NUMBER: 10/645,012
7 <141> CURRENT FILING DATE: 2003-08-21
8 <150> PRIOR APPLICATION NUMBER: US/09/700,820
9 <151> PRIOR FILING DATE: 2000-11-20
10 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02341
11 <151> PRIOR FILING DATE: 1999-04-30
12 <150> PRIOR APPLICATION NUMBER: JP 10/138652
13 <151> PRIOR FILING DATE: 1998-05-20
14 <150> PRIOR APPLICATION NUMBER: JP 10/279876
15 <151> PRIOR FILING DATE: 1998-10-01
16 <160> NUMBER OF SEQ ID NOS: 39
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 15
20 <212> TYPE: PRT
21 <213> ORGANISM: Artificial Sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: Description of Artificial Sequence:Peptide Linker Sequence
24 <400> SEQUENCE: 1
25      Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
26      1          5          10          15
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 1035
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1035)
35 <400> SEQUENCE: 2
36      atg ctg gcc gtc ggc tgc gcg ctg ctg gct gcc ctg ctg gcc gcg ccg      48
37      Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
38      1          5          10          15
39      gga gcg gcg ctg gcc cca agg cgc tgc cct gcg cag gag gtg gca aga      96
40      Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
41      20          25          30
42      ggc gtg ctg acc agt ctg cca gga gac agc gtg act ctg acc tgc ccg      144
43      Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
44      35          40          45
45      ggg gta gag ccg gaa gac aat gcc act gtt cac tgg gtg ctc agg aag      192

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46	Gly	Val	Glu	Pro	Glu	Asp	Asn	Ala	Thr	Val	His	Trp	Val	Leu	Arg	Lys	
47		50					55					60					
48	ccg	gct	gca	ggc	tcc	cac	ccc	agc	aga	tgg	gct	ggc	atg	gga	agg	agg	240
49	Pro	Ala	Ala	Gly	Ser	His	Pro	Ser	Arg	Trp	Ala	Gly	Met	Gly	Arg	Arg	
50	65					70					75					80	
51	ctg	ctg	ctg	agg	tcg	gtg	cag	ctc	cac	gac	tct	gga	aac	tat	tca	tgc	288
52	Leu	Leu	Leu	Arg	Ser	Val	Gln	Leu	His	Asp	Ser	Gly	Asn	Tyr	Ser	Cys	
53					85					90					95		
54	tac	cgg	gcc	ggc	cgc	cca	gct	ggg	act	gtg	cac	ttg	ctg	gtg	gat	gtt	336
55	Tyr	Arg	Ala	Gly	Arg	Pro	Ala	Gly	Thr	Val	His	Leu	Leu	Val	Asp	Val	
56				100					105					110			
57	ccc	ccc	gag	gag	ccc	cag	ctc	tcc	tgc	ttc	cgg	aag	agc	ccc	ctc	agc	384
58	Pro	Pro	Glu	Glu	Pro	Gln	Leu	Ser	Cys	Phe	Arg	Lys	Ser	Pro	Leu	Ser	
59			115					120					125				
60	aat	gtt	gtt	tgt	gag	tgg	ggt	cct	cgg	agc	acc	cca	tcc	ctg	acg	aca	432
61	Asn	Val	Val	Cys	Glu	Trp	Gly	Pro	Arg	Ser	Thr	Pro	Ser	Leu	Thr	Thr	
62		130					135					140					
63	aag	gct	gtg	ctc	ttg	gtg	agg	aag	ttt	cag	aac	agt	ccg	gcc	gaa	gac	480
64	Lys	Ala	Val	Leu	Leu	Val	Arg	Lys	Phe	Gln	Asn	Ser	Pro	Ala	Glu	Asp	
65	145					150					155					160	
66	ttc	cag	gag	ccg	tgc	cag	tat	tcc	cag	gag	tcc	cag	aag	ttc	tcc	tgc	528
67	Phe	Gln	Glu	Pro	Cys	Gln	Tyr	Ser	Gln	Glu	Ser	Gln	Lys	Phe	Ser	Cys	
68					165					170					175		
69	cag	tta	gca	gtc	ccg	gag	gga	gac	agc	tct	ttc	tac	ata	gtg	tcc	atg	576
70	Gln	Leu	Ala	Val	Pro	Glu	Gly	Asp	Ser	Ser	Phe	Tyr	Ile	Val	Ser	Met	
71			180						185					190			
72	tgc	gtc	gcc	agt	agt	gtc	ggg	agc	aag	ttc	agc	aaa	act	caa	acc	ttt	624
73	Cys	Val	Ala	Ser	Ser	Val	Gly	Ser	Lys	Phe	Ser	Lys	Thr	Gln	Thr	Phe	
74			195					200					205				
75	cag	ggt	tgt	gga	atc	ttg	cag	cct	gat	ccg	cct	gcc	aac	atc	aca	gtc	672
76	Gln	Gly	Cys	Gly	Ile	Leu	Gln	Pro	Asp	Pro	Pro	Ala	Asn	Ile	Thr	Val	
77		210					215					220					
78	act	gcc	gtg	gcc	aga	aac	ccc	cgc	tgg	ctc	agt	gtc	acc	tgg	caa	gac	720
79	Thr	Ala	Val	Ala	Arg	Asn	Pro	Arg	Trp	Leu	Ser	Val	Thr	Trp	Gln	Asp	
80	225					230					235					240	
81	ccc	cac	tcc	tgg	aac	tca	tct	ttc	tac	aga	cta	cgg	ttt	gag	ctc	aga	768
82	Pro	His	Ser	Trp	Asn	Ser	Ser	Phe	Tyr	Arg	Leu	Arg	Phe	Glu	Leu	Arg	
83					245					250					255		
84	tat	cgg	gct	gaa	cgg	tca	aag	aca	ttc	aca	aca	tgg	atg	gtc	aag	gac	816
85	Tyr	Arg	Ala	Glu	Arg	Ser	Lys	Thr	Phe	Thr	Thr	Trp	Met	Val	Lys	Asp	
86				260					265					270			
87	ctc	cag	cat	cac	tgt	gtc	atc	cac	gac	gcc	tgg	agc	ggc	ctg	agg	cac	864
88	Leu	Gln	His	His	Cys	Val	Ile	His	Asp	Ala	Trp	Ser	Gly	Leu	Arg	His	
89			275					280					285				
90	gtg	gtg	cag	ctt	cgt	gcc	cag	gag	gag	ttc	ggg	caa	ggc	gag	tgg	agc	912
91	Val	Val	Gln	Leu	Arg	Ala	Gln	Glu	Glu	Phe	Gly	Gln	Gly	Glu	Trp	Ser	
92		290					295					300					
93	gag	tgg	agc	ccg	gag	gcc	atg	ggc	acg	cct	tgg	aca	gaa	tcc	agg	agt	960
94	Glu	Trp	Ser	Pro	Glu	Ala	Met	Gly	Thr	Pro	Trp	Thr	Glu	Ser	Arg	Ser	

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95      305      310      315      320
96      cct cca gct gag aac gag gtg tcc acc ccc atg cag gca ctt act act      1008
97      Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr
98      325      330      335
99      aat aaa gac gat gat aat att ctc ttc      1035
100     Asn Lys Asp Asp Asp Asn Ile Leu Phe
101     340      345
103 <210> SEQ ID NO: 3
104 <211> LENGTH: 40
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Description of Artificial Sequence: "IL6R1", an artificially
synthesized primer sequence
109 <400> SEQUENCE: 3
110     ttccaattcc caccatgctg gccgtcggct gcgcgctgct      40
112 <210> SEQ ID NO: 4
113 <211> LENGTH: 36
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence: "IL6R2", an artificially
synthesized primer sequence
118 <400> SEQUENCE: 4
119     ttccaattcg aagagaatat tatcatcgtc tttatt      36
121 <210> SEQ ID NO: 5
122 <211> LENGTH: 768
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <221> NAME/KEY: CDS
127 <222> LOCATION: (1)..(768)
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Description of Artificial Sequence: a designed single chain
Fv gene sequence
130 <400> SEQUENCE: 5
131     cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga cct agc cag      48
132     Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
133     1      5      10      15
134     acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att acc agc gat      96
135     Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
136     20      25      30
137     cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt ctt gag tgg      144
138     His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
139     35      40      45
140     att gga tac att agt tat agt gga atc aca acc tat aat cca tct ctc      192
141     Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu
142     50      55      60
143     aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac cag ttc agc      240
144     Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser
145     65      70      75      80
146     ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt tat tat tgt      288

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147	Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys	
148		85 90 95
149	gca aga tcc cta gct cgg act acg gct atg gac tac tgg ggt caa ggc	336
150	Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly	
151		100 105 110
152	agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tgg ggt ggt ggt ggt	384
153	Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
154		115 120 125
155	tgc ggt ggt ggc gga tgc gac atc cag atg acc cag agc cca agc agc	432
156	Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
157		130 135 140
158	ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aga gcc agc	480
159	Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
160		145 150 155 160
161	cag gac atc agc agt tac ctg aat tgg tac cag cag aag cca gga aag	528
162	Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys	
163		165 170 175
164	gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac tct ggt gtg	576
165	Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val	
166		180 185 190
167	cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc	624
168	Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr	
169		195 200 205
170	atc agc agc ctc cag cca gag gac atc gct acc tac tac tgc caa cag	672
171	Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln	
172		210 215 220
173	ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag gtg gaa atc	720
174	Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
175		225 230 235 240
176	aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat	768
177	Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
178		245 250 255
180	<210> SEQ ID NO: 6	
181	<211> LENGTH: 32	
182	<212> TYPE: DNA	
183	<213> ORGANISM: Artificial Sequence	
184	<220> FEATURE:	
185	<223> OTHER INFORMATION: Description of Artificial Sequence: "TMT1", an artificially synthesized primer sequence	
186	<400> SEQUENCE: 6	
187	ggtgtcgtact cccaggtcca actgcaggag ag	32
189	<210> SEQ ID NO: 7	
190	<211> LENGTH: 32	
191	<212> TYPE: DNA	
192	<213> ORGANISM: Artificial Sequence	
193	<220> FEATURE:	
194	<223> OTHER INFORMATION: Description of Artificial Sequence: "LINK1", an artificially synthesized primer sequence	
195	<400> SEQUENCE: 7	
196	ctcgtcacag tctcctcagg tggtggtggt tc	32
198	<210> SEQ ID NO: 8	

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199 <211> LENGTH: 38
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK3", an artificially
synthesized primer sequence
204 <400> SEQUENCE: 8
205      gacatccaga tgacccagag cccaagcagc ctgagcgc      38
207 <210> SEQ ID NO: 9
208 <211> LENGTH: 63
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence: "SCP-C", an artificially
synthesized primer sequence
213 <400> SEQUENCE: 9
214      gctgaattct tattatttat cgtcacgctc tttgtagtca agcttatcag atggcgggaa      60
215      gat      63
217 <210> SEQ ID NO: 10
218 <211> LENGTH: 9
219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: FLAG peptide
223 <400> SEQUENCE: 10
224      Met Asp Tyr Lys Asp Asp Asp Asp Lys
225      1          5
227 <210> SEQ ID NO: 11
228 <211> LENGTH: 34
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK2", an artificially
synthesized primer sequence
233 <400> SEQUENCE: 11
234      aaccaccacc acctgaggag actgtgacga ggct      34
236 <210> SEQ ID NO: 12
237 <211> LENGTH: 35
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK4", an artificially
synthesized primer sequence
242 <400> SEQUENCE: 12
243      aggctgcttg ggctctgggt catctggatg tccga      35
245 <210> SEQ ID NO: 13
246 <211> LENGTH: 36
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence: "TMT2", an artificially
synthesized primer sequence
251 <400> SEQUENCE: 13

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252 atccggggcc gcttattatt tatcgtcac gtcttt

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : N:\Crf3\RULE60\10645012.RAW.txt
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 23
 Seq#:3; Line(s) 108
 Seq#:4; Line(s) 117
 Seq#:5; Line(s) 129
 Seq#:6; Line(s) 185
 Seq#:7; Line(s) 194
 Seq#:8; Line(s) 203
 Seq#:9; Line(s) 212
 Seq#:11; Line(s) 232
 Seq#:12; Line(s) 241
 Seq#:13; Line(s) 250
 Seq#:15; Line(s) 270
 Seq#:16; Line(s) 280
 Seq#:18; Line(s) 477
 Seq#:19; Line(s) 486
 Seq#:20; Line(s) 495
 Seq#:21; Line(s) 507
 Seq#:22; Line(s) 620
 Seq#:23; Line(s) 633
 Seq#:26; Line(s) 758
 Seq#:27; Line(s) 838
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 Seq#:29; Line(s) 927
 Seq#:30; Line(s) 940
 Seq#:31; Line(s) 1047
 Seq#:32; Line(s) 1056
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 Seq#:34; Line(s) 1077
 Seq#:35; Line(s) 1205
 Seq#:36; Line(s) 1214
 Seq#:37; Line(s) 1224
 Seq#:38; Line(s) 1233
 Seq#:39; Line(s) 1245

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/645,012

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Input Set : N:\Crf3\RULE60\10645012.RAW.txt

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L:295 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 17, CDS LOCATION:29..2839